

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:10:57 ; Search time 52.6444 Seconds
(without alignments)
740.659 Million cell updates/sec

Title: US-10-010-942B-4

Perfect score: 719

Sequence: 1 MNFGLSLIFLVVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	718	99.9	138	5	ABG76924	Abg76924 Mouse 3D6
2	652	90.7	138	5	ABG76928	Abg76928 Humanised
3	651	90.5	468	6	ABP58275	Abp58275 Humanised
4	650	90.4	138	5	ABG76932	Abg76932 Humanised
5	609.5	84.8	133	6	ABG74243	Abg74243 Mouse ant
6	578.5	80.5	139	6	ABG74247	Abg74247 Mouse ant
7	578	80.4	462	6	AAO29869	Aao29869 Mouse ant
8	578	80.4	464	5	AAU72801	Aau72801 TRA-8 hea
9	573	79.7	138	2	AAR20064	Aar20064 MRK16-H c

10	569	79.1	144	5	ABB79730	Abb79730 Anti-Stre
11	568	79.0	139	2	AAR30480	Aar30480 hCEA spec
12	566	78.7	140	5	AAU76122	Aau76122 Mouse mon
13	564	78.4	139	2	AAR27053	Aar27053 Anti-CEA
14	564	78.4	140	5	AAU76133	Aau76133 Mouse mAb
15	563	78.3	138	2	AAW03722	Aaw03722 Anti-huma
16	561	78.0	140	5	AAU76132	Aau76132 Mouse mAb
17	560	77.9	138	3	AYY32404	Aay32404 Mouse ant
18	559	77.7	140	6	ABG74241	Abg74241 Mouse ant
19	557.5	77.5	137	2	AAW57592	Aaw57592 Chimeric
20	557.5	77.5	137	2	AAW89625	Aaw89625 Mouse hum
21	557.5	77.5	137	3	AYY77513	Aay77513 Mouse ant
22	557.5	77.5	137	4	AAG67102	Aag67102 Amino aci
23	557.5	77.5	137	4	AAG64775	Aag64775 Mouse ant
24	557.5	77.5	137	4	AAG63393	Aag63393 Amino aci
25	557.5	77.5	137	5	ABB95208	Abb95208 Mouse joi
26	557.5	77.5	137	6	ABJ36667	Abj36667 Angiogene
27	557	77.5	119	6	ABP58271	Abp58271 Humanised
28	557	77.5	449	6	ABP58273	Abp58273 Humanised
29	554.5	77.1	139	1	AAP90480	Aap90480 Chimeric
30	551	76.6	119	6	ABP58269	Abp58269 Humanised
31	551	76.6	158	2	AAW19579	Aaw19579 Mouse ant
32	551	76.6	477	2	AAR47450	Aar47450 T84.12 He
33	551	76.6	477	2	AAR47453	Aar47453 chiT84.12
34	549	76.4	140	2	AAW21841	Aaw21841 Heavy cha
35	549	76.4	247	2	AAW11917	Aaw11917 Murine MA
36	545	75.8	142	2	AAR30882	Aar30882 Antibody
37	542	75.4	140	7	ADC24966	Adc24966 Murine G2
38	539	75.0	136	2	AAR06251	Aar06251 Variable
39	539	75.0	138	3	AYY32406	Aay32406 Mouse ant
40	537	74.7	159	4	AAU14226	Aau14226 Human nov
41	535	74.4	138	2	AAR32246	Aar32246 BR55-2 mu
42	535	74.4	138	2	AAR32242	Aar32242 Chimeric
43	535	74.4	139	2	AAR31588	Aar31588 BR55-2 he
44	535	74.4	158	2	AAW19577	Aaw19577 Mouse ant
45	534.5	74.3	139	2	AAR52773	Aar52773 Murine KC

ALIGNMENTS

RESULT 1

ABG76924

ID ABG76924 standard; protein; 138 AA.

XX

AC ABG76924;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VH protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX
OS Mus musculus.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
DR N-PSDB; ABS59427.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 68; Fig 2; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 138 AA;

Query Match 99.9%; Score 718; DB 5; Length 138;
Best Local Similarity 99.3%; Pred. No. 5.4e-57;
Matches 137; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
Db 121 YSGSSDYWGQGTTITVSS 138

RESULT 2
ABG76928

ID ABG76928 standard; protein; 138 AA.
XX
AC ABG76928;
XX
DT 05-NOV-2002 (first entry)
XX
DE Humanised 3D6 heavy chain variable region #1.
XX
KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 54; Page 155; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention
XX
SQ Sequence 138 AA;

Query Match 90.7%; Score 652; DB 5; Length 138;
Best Local Similarity 89.1%; Pred. No. 4.8e-51;
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
		: : : : :	
Db	1	MNFGLSLIFLVLVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP	60
Qy	61	DKRLEWVASIRSGGGRTYYSDNVKGRFTISRNEAKNTLYLQMSSLKSEDTALYYCVRYDH	120
		: : : :	
Db	61	GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCVRYDH	120
Qy	121	YSGSSDYWGQGTTVTVSS	138
Db	121	YSGSSDYWGQGTLVTVSS	138

RESULT 3
ABP58275
ID ABP58275 standard; protein; 468 AA.
XX
AC ABP58275;
XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 3D6 antibody heavy chain.
XX
KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
KW human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .468
FT /label= Mature_peptide
FT /note= "the mature heavy chain is claimed in Claim 5"
FT Region 20. .138
FT /note= "heavy chain variable region, claimed in Claim 4"
FT Region 50. .54
FT /note= "CDR1"
FT Region 69. .85
FT /note= "CDR2"
FT Region 118. .127
FT /note= "CDR3"
XX
PN WO200288306-A2.
XX
PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011853.
XX
PR 30-APR-2001; 2001US-0287539P.
XX
PA (ELIL) LILLY & CO ELI.
XX

PI Tsurushita N, Vasquez M;
XX
DR WPI; 2003-183835/18.
DR N-PSDB; ABZ24633, ABZ24635.
XX
PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plaque in the brain.
XX
PS Disclosure; Page 13-14; 54pp; English.
XX
CC The present sequence is that of a preferred heavy chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline VH segment DP-45 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 468 AA;

Query Match 90.5%; Score 651; DB 6; Length 468;
Best Local Similarity 89.1%; Pred. No. 2.4e-50;
Matches 123; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy	1	MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
		: : :	
Db	1	MNFGLSLIFLVLVLKGVQCEVQLVESGGGLVQPGGSLRLSCAGSGFTFSNYGMSWVRQAP	60
Qy	61	DKRLEWVASIRSGGGRTYYSDNVKGRTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH	120
		: : : :	
Db	61	GKGLEWVASIRSGGGRTYYSDNVKGRTISRENAKNSLYLQMNSLRAEDTAVYYCVRYDH	120
Qy	121	YSGSSDYWGQGTTVTVSS	138
Db	121	YSGSSDYWGQGTLVTVSS	138

RESULT 4
ABG76932
ID ABG76932 standard; protein; 138 AA.
XX
AC ABG76932;
XX
DT 05-NOV-2002 (first entry)
XX
DE Humanised 3D6 heavy chain variable region #2.

XX
KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 55; Page 157; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention
XX
SQ Sequence 138 AA;

Query Match 90.4%; Score 650; DB 5; Length 138;
Best Local Similarity 88.4%; Pred. No. 7.3e-51;
Matches 122; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:|||||:|||||:|||||:|:|||||:||| ||:|||||:|||||:|||||:|||||:
Db 1 MNFGLSLIFLVVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
|:|||||:|||||:|||||:|||||:|:|||||:|||:|||||:
Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRYDH 120

Qy	121	YSGSSDYWGQGTTVTVSS	138
Db	121	YSGSSDYWGQGTLTVTVSS	138

RESULT 5
ABG74243
ID ABG74243 standard; protein; 133 AA.
XX
AC ABG74243;
XX
DT 22-APR-2003 (first entry)
XX
DE Mouse antibody 3D8 heavy chain variable region.
XX
KW T-cell receptor; cytostatic; dermatological; neuroprotective;
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW small cell lung cancer; heavy chain variable region; mouse.
XX
OS Mus sp.
XX
PN US2002132983-A1.
XX
PD 19-SEP-2002.
XX
PF 10-DEC-2001; 2001US-00006773.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-208946/20.
DR N-PSDB; ABX16569.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 12; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to

CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC represents the mouse antibody 3D8 heavy chain variable region
XX

SQ Sequence 133 AA;

Query Match 84.8%; Score 609.5; DB 6; Length 133;
Best Local Similarity 87.0%; Pred. No. 3.1e-47;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

Db 1 MNFGLSLIFLVLVLKGVCQCEVKVVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
|||:|||||:|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||:|

Db 61 DKRLEWVASISSSGGDSTFYADNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCARDL 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
:::|||||:|||||

Db 121 FN----WGQGTTLTVSS 133

RESULT 6

ABG74247

ID ABG74247 standard; protein; 139 AA.

XX

AC ABG74247;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3E11 heavy chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW small cell lung cancer; heavy chain variable region; mouse.

XX

OS Mus sp.

XX

PN US2002132983-A1.

XX

PD 19-SEP-2002.

XX

PF 10-DEC-2001; 2001US-00006773.

XX

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX

PA (JUNG/) JUNGHANS R P.

XX

PI Junghans RP;

XX

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16573.

XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 17; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC represents the mouse antibody 3E11 heavy chain variable region
XX
SQ Sequence 139 AA;

Query Match 80.5%; Score 578.5; DB 6; Length 139;
Best Local Similarity 82.7%; Pred. No. 2e-44;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| ||||||| ||| ||| ||| ||| ||| ||| :|: ||| ||| ||| ||| :| ||| ||| ||| ||| |
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSFSNYGMSWVRQTS 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||||||| ||| :||| :||| ||| ||| ||| ||| ||| ||| ||| ||| :||| ||| | | |
Db 61 DKRLEWVASISTGGANTFYPDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYFCARDSH 120

Qy 121 YSGS-SDYWGQGTTTVVSS 138
| ||||| ||||:
Db 121 SVGCWFATWGQGTLVTVSA 139

RESULT 7
AAO29869
ID AAO29869 standard; protein; 462 AA.
XX
AC AAO29869;
XX
DT 27-AUG-2003 (first entry)
XX
DE Mouse anti-human DR5 antibody (TRA-8) heavy chain.
XX
KW Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;

KW Crohn's disease; diabetes mellitus; antibody; mouse.
XX
OS Mus sp.
XX
PN WO2003037913-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035333.
XX
PR 01-NOV-2001; 2001US-0346402P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX
DR WPI; 2003-441350/41.
DR N-PSDB; AAL60477.
XX
PT New purified antibody that specifically binds a TNF-related apoptosis-inducing ligand receptor DR4 or DR5, useful for treating cancer, inflammatory disease or autoimmune disease in a subject, e.g. asthma or rheumatoid arthritis.
XX
PS Example 16; Page 224-225; 251pp; English.
XX
CC The invention relates to an antibody that specifically binds a tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor DR4 or DR5. Antibodies of the invention are useful for selectively inducing apoptosis in target cells expressing DR4, for inhibiting proliferation of target cells expressing DR4 or for treating cancer, inflammatory disease or autoimmune disease in a subject e.g. systemic lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or glomerular nephritis. The present sequence is mouse anti-human DR5 antibody (TRA-8) heavy chain
XX
SQ Sequence 462 AA;

Query Match 80.4%; Score 578; DB 6; Length 462;
Best Local Similarity 81.2%; Pred. No. 8.8e-44;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 EKRLEWVATISSLGGSYTYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGD 120
Qy 121 YSGSSDYWGQGTTVTVSS 138
Db 121 SMITTDYWGQGTTLTVSS 138

RESULT 8
AAU72801
ID AAU72801 standard; protein; 464 AA.
XX
AC AAU72801;
XX
DT 26-FEB-2002 (first entry)
XX
DE TRA-8 heavy chain.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Mus musculus.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014151.
XX
PR 02-MAY-2000; 2000US-0201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI; 2002-049338/06.
DR N-PSDB; AAS97062.
XX
PT Novel antibody specific for tumor necrosis factor-related apoptosis-
PT inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS Claim 26; Page 198-199; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular

CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. Peptides used to design primers for isolating heavy and
CC light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
CC shown in AAU72799 and AAU72800

XX

SQ Sequence 464 AA;

Query Match 80.4%; Score 578; DB 5; Length 464;
Best Local Similarity 81.2%; Pred. No. 8.9e-44;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASILKLSCAASGFTFSNYGMSWVRQNS 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :| ||| |||

Db 1 MNFGLSLIFLVVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
:| | | | | | :| ||| ||| | :| | | | | | | | | | | | | | | | | | | | | | |

Db 61 EKRLEWVATISSLGGSYTYYPDSDKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGD 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
::| | | | | | :| | | |

Db 121 SMITTDYWGQGTTLVSS 138

RESULT 9

AAR20064

ID AAR20064 standard; protein; 138 AA.

XX

AC AAR20064;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 27-MAR-1992 (first entry)

XX

DE MRK16-H chain.

XX

KW Monoclonal antibody; light; heavy; chain; cancer; drug resistance.

XX

OS Homo; sapiens.

OS Mus musculus.

OS Chimeric.

XX

PN JP03254691-A.

XX

PD 13-NOV-1991.

XX

PF 02-MAR-1990; 90JP-00051563.

XX

PR 02-MAR-1990; 90JP-00051563.

XX

PA (GANK-) ZH GAN KENKYUKAI.

PA (FUJI-) FUJITA GAKUEN GH.

PA (NICA-) JAPAN FOUND CANCER RES.

XX

DR WPI; 1992-002461/01.

DR N-PSDB; AAQ20070.

XX
PT Chimera antibody against drug resistant cancer - comprises variable
PT region homologous to region in mouse monoclonal antibody and constant
PT region homologous to region in human immunoglobulin.
XX
PS Disclosure; Fig 4; 20pp; Japanese.
XX
CC A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MRK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 138 AA;

Query Match 79.7%; Score 573; DB 2; Length 138;
Best Local Similarity 80.4%; Pred. No. 6.3e-44;
Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db |||||||:||||| ||||||| ||||||| |||||||:|| |||||
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db :|||||:| ||||| ||| :|||||:||| |||||||:||||| |||
Qy 121 YSGSSDYWGQGTTVTVSS 138
Db | ||||| ||||:
Qy 121 YEAWFASWGQGTLTVSA 138

RESULT 10
ABB79730
ID ABB79730 standard; protein; 144 AA.
XX
AC ABB79730;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.
XX
KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy.
XX
OS Mus musculus.
XX
PN US2002068066-A1.
XX
PD 06-JUN-2002.
XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

DR WPI; 2002-565838/60.

DR N-PSDB; ABN84611.

XX

PT Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified

PT antibodies that bind to surface antigens of carcinogenic organisms.

XX

PS Claim 14; Fig 3B; 30pp; English.

XX

CC The present sequence is the protein sequence of the heavy chain variable
CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion

XX

SQ Sequence 144 AA;

Query Match 79.1%; Score 569; DB 5; Length 144;

Best Local Similarity 78.2%; Pred. No. 1.5e-43;

Matches 111; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:|||||:||||| ||||||:|||||||||| |||||||||||:| |||||

Db 1 MDFGLSLVFLVTLKGVQCDVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
:||||||||| ||| ||| :|||||||||:|||||||||:|||||||:||| |

Db 61 EKRLEWVASISSLGGTYTYYPDSVKGRFTISRDNAKNTLYLQMTSLKSEDTAMYCSRDDG 120

Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138

| | :|||||||:|||||

Db 121 SYGSYYYAMDYWGQGTSVTVSS 142

RESULT 11

AAR30480

ID AAR30480 standard; protein; 139 AA.

XX
AC AAR30480;
XX
DT 06-MAY-1993 (first entry)
XX
DE hCEA specific mouse heavy chain variable chain region.
XX
KW Chimeric antibody; human cancer embryonal antigen; treatment; diagnosis;
KW cancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /note= "signal peptide"
FT Protein 20. .139
FT /note= "mature peptide"
XX
PN JP04330295-A.
XX
PD 18-NOV-1992.
XX
PF 28-DEC-1990; 90JP-00408811.
XX
PR 28-DEC-1990; 90JP-00408811.
XX
PA (MITU) MITSUBISHI KASEI CORP.
XX
DR WPI; 1993-003502/01.
DR N-PSDB; AAQ33052.
XX
PT Mouse-human chimeric antibody for diagnosis and treatment of cancer -
PT obtd. by combining variable region of mouse antibody specifically
PT combining to human cancer embryonic antigen with constant region of human
PT antibody.
XX
PS Disclosure; Page 6; 10pp; Japanese.
XX
CC The sequence is that of the heavy chain variable region of a mouse
CC antibody specific to human cancer embryonal antigen (hCEA). The region is
CC used, with the corresponding mouse light chain variable region and the
CC constant region of a human antibody, to prepare a mouse-human chimeric
CC antibody which can be used for the diagnosis and treatment of cancer
XX
SQ Sequence 139 AA;

Query Match 79.0%; Score 568; DB 2; Length 139;
Best Local Similarity 80.6%; Pred. No. 1.8e-43;
Matches 112; Conservative 10; Mismatches 15; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 EKRLEWVASITSQGS-TYYPDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARVHY 119

Qy 121 Y-SGSSDYWGQGTTTVSS 138
| | : |||||:|||||
Db 120 YDSPAMDYWGQGTSVTVSS 138

RESULT 12
AAU76122
ID AAU76122 standard; protein; 140 AA.
XX
AC AAU76122;
XX
DT 08-MAY-2002 (first entry)
XX
DE Mouse monoclonal antibody 26-2F heavy chain variable region.
XX
KW Mouse; monoclonal antibody; heavy chain variable region; VH; angiogenin;
KW 26-2F; angiogenesis; tumour; cancer; retinopathy;
KW ocular neovascular disease; vitamin A deficiency; syphilis;
KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;
KW sickle cell anaemia; Paget's disease; mycobacterial infection;
KW osteoarthritis; graft versus host disease; autoimmune disease;
KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;
KW myasthenia gravis.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .140
FT /label= Mature_VH
FT Region 50. .54
FT /label= Complementarity_determining_region
FT /note= "This region is specifically claimed in claim 3"
FT Region 69. .85
FT /label= Complementarity_determining_region
FT /note= "This region is specifically claimed in claim 3"
FT Region 118. .129
FT /label= Complementarity_determining_region
FT /note= "This region is specifically claimed in claim 3"
XX
PN US2002010320-A1.
XX
PD 24-JAN-2002.
XX
PF 05-APR-1999; 99US-00286240.
XX
PR 05-APR-1999; 99US-00286240.
XX
PA (FETT/) FETT J W.
XX
PI Fett JW;
XX
DR WPI; 2002-187790/24.
DR N-PSDB; ABK15270.
XX

PT New antibody immunologically reactive to angiogenin useful for inhibiting angiogenesis and for treating conditions associated with abnormal angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid arthritis.

XX

PS Claim 6; Page 14; 20pp; English.

XX

CC The invention relates to an antibody immunologically reactive to angiogenin or a fragment of angiogenin comprising light and heavy chain nonhuman-derived complementarity determining regions having a binding affinity to the angiogenin or its fragment in combination with human derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also included are an expression vector comprising a nucleic acid encoding the antibody and a host cell transformed with the vector. The antibody or its fragment is useful for inhibiting the angiogenic activity of angiogenin. The antibody is useful for treating a tumour in humans, by inhibiting, prohibiting, reducing or eliminating a tumour growth, or inhibiting the ability of circulating tumour cell to form a vascularised tumour mass. The antibody is useful for treating a mammal with abnormal or unwanted angiogenesis, including cancer, and other diseases mediated by angiogenesis, including ocular neovascular disease, diabetic retinopathy, retinopathy of prematurity, corneal graft rejection, neovascular glaucoma and retrothalic fibroplasia, and other diseases associated with corneal neovascularisation including epidemic keratoconjunctivitis, vitamin A deficiency, contact lens overwear, atopic keratitis, superior limbic keratitis, syphilis, mycobacteria infections, lipid degeneration, chemical burns, bacterial ulcers, fungal ulcers, herpes simplex infections, herpes zoster infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma, Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal graft rejection. Diseases associated with retinal/choroidal neovascularisation include macular degeneration, sickle cell anaemia, sarcoid, Paget's disease, mycobacterial infections, Bechets disease, trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host disease, transplant rejection, autoimmune diseases such as type I diabetes, multiple sclerosis, systemic lupus erythematosus, and myasthenia gravis. The present sequence is the heavy chain variable region of mouse monoclonal antibody 26-2F

XX

SQ Sequence 140 AA;

Query Match 78.7%; Score 566; DB 5; Length 140;
Best Local Similarity 79.3%; Pred. No. 2.7e-43;
Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:|||| :||||:||||||| ||||||||| |||||||||:| |||||

Db 1 MDFGLSWVFLVLILKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY-D 119
:|||||||:| ||||| ||| :|||||||:| |||||||||:||||||| | |

Db 61 EKRLEWVATISSGGGNTYYPDSDKGRFTISRDIAKNTLYLQMSSLRSEDTALYYCTRLGD 120

Qy 120 H-YSGSSDYWGQGTTVTVSS 138
: | : : |||||||:|||||

Db 121 YGYAYTMDYWGQGTSVTVSS 140

RESULT 13

AAR27053

ID AAR27053 standard; protein; 139 AA.

XX

AC AAR27053;

XX

DT 01-MAR-1993 (first entry)

XX

DE Anti-CEA specific heavy chain variable region.

XX

KW Human; carcinoembryonic antigen; heavy chain; light chain; variable; region; diagnostic; tumour; markers; targetting.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /note= "signal peptide"

FT Protein 20. .139

FT /note= "mature peptide"

XX

PN JP04234987-A.

XX

PD 24-AUG-1992.

XX

PF 28-DEC-1990; 90JP-00408810.

XX

PR 28-DEC-1990; 90JP-00408810.

XX

PA (MITU) MITSUBISHI KASEI CORP.

XX

DR WPI; 1992-327631/40.

DR N-PSDB; AAQ28746.

XX

PT New DNA fragments encoding variable regions of ABS specific for human CEA
PT - for diagnosing and monitoring tumours, as tumour markers and for
PT treatment of tumours.

XX

PS Disclosure; Fig 1; 7pp; Japanese.

XX

CC The anti-CEA murine monoclonal antibody heavy chain variable region was
CC obtd. by screening a cDNA library prep'd. from mRNA obtd. from hybridomas
CC producing anti-CEA-specific antibodies with a probe based on the constant
CC region of the H-chain. The antibodies reacts specifically with human CEA
CC and are useful as a diagnostic agents, as tumour markers for digestive
CC organs, for diagnosis of malignant tumours; for monitoring after cancer
CC operations, to follow up bloodless therapy or as therapeutic agents in
CC passive immune therapy and targetting therapy. See also AAR27054

XX

SQ Sequence 139 AA;

Query Match 78.4%; Score 564; DB 2; Length 139;

Best Local Similarity 79.9%; Pred. No. 4.1e-43;

Matches 111; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Db ||||| ||||||||||||||||||||||||||| |||||||||||||||:| |||||
1 MNFGFSLIFLVVLKGVQCEVKLVESGGGLVKPGGSLKLSAASGFTFSSYAMSWVRQTP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
:||||||||| | | | |:|||||||:|||:| | | | | |:|||:||| | :
Db 61 EKRLEWVASITSDGS-TYYPDGVKGRFTISRDNARNILYLQMSSLRSEETAMYYCARVHY 119
Qy 121 Y-SGSSDYWGQGTTVTVSS 138
| | : | | | | |:| | | |
Db 120 YDSPAMDYWGQGTSVTVSS 138

RESULT 14

AAU76133

ID AAU76133 standard; protein; 140 AA.

XX

AC AAU76133;

XX

DT 08-MAY-2002 (first entry)

XX

DE Mouse mAb 26-2F heavy chain variable region mutant E59Y.

XX

KW Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy;
KW ocular neovascular disease; vitamin A deficiency; syphilis;
KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;
KW sickle cell anaemia; Paget's disease; mycobacterial infection;
KW osteoarthritis; graft versus host disease; autoimmune disease;
KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;
KW myasthenia gravis; mutant; mutein; monoclonal antibody; 26-2F;
KW heavy chain variable region; E59Y.

XX

OS Mus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /label= Signal_peptide

FT Protein 20. .140

FT /label= Mature_VH

FT Misc-difference 59

FT /note= "Wild-type Glu substituted by Tyr"

XX

PN US2002010320-A1.

XX

PD 24-JAN-2002.

XX

PF 05-APR-1999; 99US-00286240.

XX

PR 05-APR-1999; 99US-00286240.

XX

PA (FETT/) FETT J W.

XX

PI Fett JW;

XX

DR WPI; 2002-187790/24.

XX

PT New antibody immunologically reactive to angiogenin useful for inhibiting

PT angiogenesis and for treating conditions associated with abnormal
PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
PT arthritis.

XX

PS Claim 11; Page; 20pp; English.

XX

CC The invention relates to an antibody immunologically reactive to
CC angiogenin or a fragment of angiogenin comprising light and heavy chain
CC nonhuman-derived complementarity determining regions having a binding
CC affinity to the angiogenin or its fragment in combination with human
CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
CC included are an expression vector comprising a nucleic acid encoding the
CC antibody and a host cell transformed with the vector. The antibody or its
CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
CC The antibody is useful for treating a tumour in humans, by inhibiting,
CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
CC ability of circulating tumour cell to form a vascularised tumour mass.
CC The antibody is useful for treating a mammal with abnormal or unwanted
CC angiogenesis, including cancer, and other diseases mediated by
CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,
CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
CC and retrothalic fibroplasia, and other diseases associated with corneal
CC neovascularisation including epidemic keratoconjunctivitis, vitamin A
CC deficiency, contact lens overwear, atopic keratitis, superior limbic
CC keratitis, syphilis, mycobacteria infections, lipid degeneration,
CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
CC infections, herpes zoster infections, protozoan infections, Kaposi's
CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal
CC graft rejection. Diseases associated with retinal/choroidal
CC neovascularisation include macular degeneration, sickle cell anaemia,
CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,
CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
CC disease, transplant rejection, autoimmune diseases such as type I
CC diabetes, multiple sclerosis, systemic lupus erythematosus, and
CC myasthenia gravis. The present sequence represents the E59Y mutant of the
CC mouse monoclonal antibody 26-2F light chain variable region. Note: The
CC present sequence is not shown in the specification but was created by the
CC indexer using the sequence appearing as AAU76122 and the information in
CC the claims

XX

SQ Sequence 140 AA;

Query Match 78.4%; Score 564; DB 5; Length 140;
Best Local Similarity 79.3%; Pred. No. 4.2e-43;
Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASILKLSCAAAGFTFSNYGMSWVRQNS 60
|:|||| :||||:||||||| ||||||||||| |||||||||||:| |||||
Db 1 MDFGLSWVFLVLILKGVQCEVMLVESGGGLVKPGGSLKLSCAAAGFTFSSYTMSWVRQYP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRTTISRENAKNTLYLQMSSLKSEDTALYYCVRY-D 119
:||||||:| |||| ||| :|||||||: |||||||||||:||||||| | |
Db 61 EKRLEWVATISSGGGNTYYPDSDKGRFTISRDIAKNTLYLQMSSLRSEDTALYYCTRLGD 120

Qy 120 H-YSGSSDYWGQGTTVTVSS 138
: |: : |||||||:|||||

RESULT 15

AAW03722

ID AAW03722 standard; protein; 138 AA.

XX

AC AAW03722;

XX

DT 02-APR-1997 (first entry)

XX

DE Anti-human gp39 MAb 39-1.106 heavy chain variable region.

XX

KW Heavy chain; variable region; murine; mouse; anti-human; disease; glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma; diagnosis; inhibition; B-cell; activation; treatment; disorder; immune; autoimmune; allergic response; organ rejection; drug; graft versus host; cell imaging; tumour; targetted; delivery; targeted.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /label= sig_peptide

FT Peptide 20. .138

FT /label= mat_peptide

FT Region 50. .54

FT /note= "complementarity determining region 1"

FT Region 69. .84

FT /note= "complementarity determining region 2"

FT Region 117. .126

FT /note= "complementarity determining region 3"

XX

PN WO9623071-A2.

XX

PD 01-AUG-1996.

XX

PF 26-JAN-1996; 96WO-US001119.

XX

PR 26-JAN-1995; 95US-00379057.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Siadak A, Hollenbaugh D, Gilliland LK, Gordon ML, Bajorath J;

PI Aruffo AA, Harris LJ;

XX

DR WPI; 1996-362694/36.

DR N-PSDB; AAT35974.

XX

PT Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc. .

XX

PS Claim 91; Fig 6B; 167pp; English.

XX

CC The present sequence is the heavy chain variable region of the murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) 39-1.106 (a

CC member of the murine III(D) subgroup). The MAb was prep'd. by immunising a
CC 6-8 week old BALB/c mouse with a gp39-CD8 fusion protein, and 3 days
CC later harvesting and fusing spleen and lymph cells to mouse melanoma
CC cells, to produce an anti-human gp39 MAb producing hybridoma. The MAb may
CC be useful for diagnosing disease states, inhibiting B-cell activation and
CC for treating immunological disorders, e.g. autoimmune disorders, allergic
CC responses, organ rejection and graft versus host disease. It may also be
CC used for imaging cells which express gp39 on their surface, e.g. tumour
CC cells, and to target therapeutic agents to such cells. The MAb inhibits
CC the CD40/gp39 interaction, therefore limiting both prim. and sec.
CC responses to T-cell dependent antigens and Ab prodn. specific to these
CC antigens. A typical compsn. for intramuscular injection pref. contains 50
CC mg of MAb in 1 ml of sterile buffered water

XX

SQ Sequence 138 AA;

Query Match 78.3%; Score 563; DB 2; Length 138;
Best Local Similarity 79.1%; Pred. No. 5e-43;
Matches 110; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||||||||||||||||||||||||| ||||| |||||:||| |||||

Db 1 MNFGFSLIFLVVLKGVQCEVKLVESGGGLVKPGGSLKLSCTTSGFTFNNYAMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR-YD 119
:||||| ||| | | ||| |:|||:|||||:|||:| |||||||:|||||:||| | ||

Db 61 EKRLEWVASI-SSGDSTYYPDSVRGRFTISRDNARNILYLQMSSLRSEDTAMYCARHYD 119

Qy 120 HYSGSSDYWGQGTTVTVSS 138

: | : |||||||:|||||

Db 120 YDSYAMDYWGQGTSVTVSS 138

Search completed: May 17, 2004, 11:30:35

Job time : 54.6444 secs

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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:29:03 ; Search time 16.8667 Seconds
(without alignments)
422.394 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719

Sequence: 1. MNFGLSLIFLVVLKGVQCE. DHYSGSSDYWGQQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	566.5	78.8	135	3	US-08-579-378A-16	Sequence 16, Appl
2	563	78.3	138	2	US-08-379-057-14	Sequence 14, Appl
3	551	76.6	158	2	US-08-653-402B-6	Sequence 6, Appl
4	549	76.4	140	3	US-08-836-561-23	Sequence 23, Appl
5	549	76.4	140	4	US-09-434-122-23	Sequence 23, Appl
6	549	76.4	247	5	PCT-US94-07659-2	Sequence 2, Appl
7	545.5	75.9	135	3	US-08-579-378A-20	Sequence 20, Appl
8	541	75.2	136	4	US-08-976-183A-33	Sequence 33, Appl
9	540	75.1	136	4	US-08-976-183A-31	Sequence 31, Appl
10	537	74.7	136	4	US-08-976-183A-32	Sequence 32, Appl
11	536	74.5	136	4	US-08-976-183A-34	Sequence 34, Appl

12	535	74.4	136	1	US-08-253-877C-57	Sequence 57, Appl
13	535	74.4	136	2	US-08-452-164A-57	Sequence 57, Appl
14	535	74.4	138	1	US-08-053-171-7	Sequence 7, Appl
15	535	74.4	138	1	US-08-053-171-11	Sequence 11, Appl
16	535	74.4	158	2	US-08-653-402B-10	Sequence 10, Appl
17	514.5	71.6	139	1	US-08-129-930B-96	Sequence 96, Appl
18	514.5	71.6	139	3	US-08-134-346A-51	Sequence 51, Appl
19	514.5	71.6	139	4	US-08-976-288A-96	Sequence 96, Appl
20	513	71.3	170	2	US-08-652-558-40	Sequence 40, Appl
21	512.5	71.3	159	2	US-08-653-402B-2	Sequence 2, Appl
22	497.5	69.2	255	2	US-07-690-192-4	Sequence 4, Appl
23	494.5	68.8	463	4	US-09-472-087-1	Sequence 1, Appl
24	494.5	68.8	463	4	US-09-472-087-63	Sequence 63, Appl
25	494.5	68.8	463	4	US-09-472-087-64	Sequence 64, Appl
26	493	68.6	464	4	US-09-472-087-2	Sequence 2, Appl
27	493	68.6	464	4	US-09-472-087-66	Sequence 66, Appl
28	490.5	68.2	135	5	PCT-US95-07302-8	Sequence 8, Appl
29	486	67.6	130	4	US-09-225-322B-8	Sequence 8, Appl
30	486	67.6	130	4	US-09-764-304-8	Sequence 8, Appl
31	484.5	67.4	122	1	US-07-634-278-48	Sequence 48, Appl
32	484.5	67.4	122	1	US-08-477-728-48	Sequence 48, Appl
33	484.5	67.4	122	1	US-08-474-040-48	Sequence 48, Appl
34	484.5	67.4	122	1	US-08-487-200-48	Sequence 48, Appl
35	484.5	67.4	122	3	US-08-484-537-48	Sequence 48, Appl
36	484	67.3	130	4	US-09-225-322B-18	Sequence 18, Appl
37	484	67.3	130	4	US-09-764-304-18	Sequence 18, Appl
38	482.5	67.1	135	3	US-08-619-491-8	Sequence 8, Appl
39	482.5	67.1	463	4	US-09-472-087-4	Sequence 4, Appl
40	482.5	67.1	463	4	US-09-472-087-68	Sequence 68, Appl
41	480.5	66.8	456	4	US-09-495-880A-11	Sequence 11, Appl
42	478.5	66.6	135	3	US-08-619-491-4	Sequence 4, Appl
43	478.5	66.6	135	5	PCT-US95-07302-4	Sequence 4, Appl
44	477	66.3	239	2	US-08-553-497A-18	Sequence 18, Appl
45	475	66.1	123	4	US-09-344-587-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-08-579-378A-16

; Sequence 16, Application US/08579378A

; Patent No. 6210671

; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung

; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One MarketPlaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-16

Query Match 78.8%; Score 566.5; DB 3; Length 135;
Best Local Similarity 81.2%; Pred. No. 1.1e-52;
Matches 112; Conservative 8; Mismatches 15; Indels 3; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGSSLIFLVVLKGVQCEVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 EKRLEWVASI-STGGSTYYPDSVKGRFTISRDNARNILYLMQSSLRSEDTAMYCAR--D 117

Qy 121 YSGSSDYWGQGTTVTVSS 138
Db 118 YDGYFDYWGQGTTLTVSS 135

RESULT 2
US-08-379-057-14
; Sequence 14, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.

; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their
Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-379-057-14

Query Match 78.3%; Score 563; DB 2; Length 138;
Best Local Similarity 79.1%; Pred. No. 2.7e-52;
Matches 110; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

Qy 1 MNFGLSLIPLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGFSLIPLVVLKGVQCEVKLVESGGGLVKPGCSLKLSCTTSGFTFNNYAMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR-YD 119
Db 61 EKRLEWVASI-SSGDSTYYPDSSVRGRFTISRDNARNILYLQMSSLRSEDTAMYYCARHYD 119

Qy 120 HYSGSSDYWGQQGTTVTVSS 138
Db 120 YDSYAMDYWGQQGTSVTVSS 138

RESULT 3

US-08-653-402B-6

; Sequence 6, Application US/08653402B

; Patent No. 5969107

; GENERAL INFORMATION:

; APPLICANT: CARCELLER, Ana

; APPLICANT: ROSELL, Elisabet

; APPLICANT: GOMEZ, Alicia

; APPLICANT: ADEN, Jaume

; APPLICANT: PIULATS, Jaume

; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an

; TITLE OF INVENTION: immune response against epidermal growth factor receptor.

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

; STREET: 2200 Clarendon Boulevard, Suite 1400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/653,402B

; FILING DATE: 24-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95107967.2

; FILING DATE: 26-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lebovitz, Richard M.

; REGISTRATION NUMBER: 37,067

; REFERENCE/DOCKET NUMBER: MERCK 1781

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333

; TELEFAX: 703-243-6410

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 158 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-653-402B-6

Query Match 76.6%; Score 551; DB 2; Length 158;

Best Local Similarity 77.8%; Pred. No. 5.9e-51;

Matches 112; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

 |:||||||||||| ||| |:||||||||||| | ||||||||||||| |||||

Db 1 MDFGLSLIFLVFKGVLCDVKLVESGGGLVKLGSSLKLSCAASGFTFSNYYMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY-- 118
:||||:||:| ||| ||| :|||||:|||||:|||||:|||:
Db 61 EKRLEFVAAINSNGGSTYYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCARHRG 120

Qy 119 ---DHYSG-SSDYWGQGTTVTVSS 138
| | : |||||:|||||
Db 121 RDSSGYVGYAIDYWGQGTSVTVSS 144

RESULT 4

US-08-836-561-23

; Sequence 23, Application US/08836561

; Patent No. 6018032

; GENERAL INFORMATION:

; APPLICANT: KOIKE, Masamichi

; APPLICANT: FURUYA, Akiko

; APPLICANT: NAKAMURA, Kazuyasu

; APPLICANT: IIDA, Akihiro

; APPLICANT: ANAZAWA, Hideharu

; APPLICANT: HANAI, No. 6018032uo

; APPLICANT: TAKATSU, Kiyoshi

; TITLE OF INVENTION: Antibody Against Human Interleukin-5

; TITLE OF INVENTION: Receptor Alpha Chain

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,561

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 232384/95

; FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lawrence, III, Stanton T

; REGISTRATION NUMBER: 25,736

; REFERENCE/DOCKET NUMBER: 7005-115-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 140 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-434-122-23

Query Match 76.4%; Score 549; DB 4; Length 140;
Best Local Similarity 74.3%; Pred. No. 8.3e-51;
Matches 104; Conservative 16; Mismatches 18; Indels 2; Gaps 1;
Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFLALILKGVQCEVQLVESGGDLVKPGGSLKLSCAASGFTFSDYGMWIRQIS 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 DKRPEWVAAISSGGSYIHFPDSLKGRFTVSRDNAKNTLYLEMSGLKSEDTAMYYCARRGF 120
Qy 121 YSG--SSDYWGQGTTVTVSS 138
Db 121 YGNYRAMDYWGQGTSVTVSS 140

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 76.4%; Score 549; DB 5; Length 247;
Best Local Similarity 78.3%; Pred. No. 1.7e-50;
Matches 108; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MNFGLRLIFLVLTKGVKCEVHLVESGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy 61 DKRLEWVVASIRSGGGRTYYSDNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
: ||| : ||| | ||| | ||| | ||| ||| ||| : ||| ||| ||| ||| ||| ||| : | |
Db 61 EKRLDWVAYISSGGGGTYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYHCARGGV 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
| | | | ||| |||
Db 121 RRGYFDVWGAGTTVTVSS 138

RESULT 7

US-08-579-378A-20

; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One MarketPlaza, Steuart Tower, Suite 2000

;
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
;
; INFORMATION FOR SEQ ID NO: 20:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-579-378A-20

Query Match 75.9%; Score 545.5; DB 3; Length 135;
Best Local Similarity 79.0%; Pred. No. 1.9e-50;
Matches 109; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60 .
||| ||||| ||||| ||||| :||| ||||| :||| ||| :||| ||||| ||| |||||
Db 1 MNFGSSLIFLVVLKGVCQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||||| | | | | | :||| ||||| :||| ||||| :||| :| | | | |
Db 61 GKGLEWVASI-STGGSTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAR--D 117

Qy 121 YSGSSDYWGQGTTVTVSS 138
| | | ||||| | | | |
Db 118 YDGYFDYWGQGTLVTVSS 135

RESULT 8

US-08-976-183A-33

; Sequence 33, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

; APPLICANT: King, David J.

; APPLICANT: Adair, John R.

; APPLICANT: Owens, Raymond J.

; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K. Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/976,183A

; FILING DATE:

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,848

; FILING DATE: 02-FEB-1996

; APPLICATION NUMBER: PCT/GB93/02529

; FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9225853.2

; FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9315249.4

; FILING DATE: 22-JUL-1993

ATTORNEY/AGENT INFORMATION:

; NAME: Bernhard D. Saxe

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 40283/151/CARA

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELEX: 904136

INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 136 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-976-183A-33

Query Match 75.2%; Score 541; DB 4; Length 136;

Best Local Similarity 75.5%; Pred. No. 5.7e-50;

Matches 108; Conservative 10; Mismatches 13; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCHAASGFTFSNYGMSWVRQNS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MNFGLSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFATSYDMSWVRQTP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC---- 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTV 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 116 VRYDHYSGSSDYWGQGTTVTVSS 138
| : ||||| |||||:
Db 121 VPF-----AYWGQGTLTVSA 136

RESULT 9

US-08-976-183A-31

; Sequence 31, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-976-183A-31

Query Match 75.1%; Score 540; DB 4; Length 136;
Best Local Similarity 74.8%; Pred. No. 7.2e-50;
Matches 107; Conservative 11; Mismatches 13; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60
|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 DKRLEWVVASIRSGGGRTYYSDNVKGRTISRENAKNTLYLQMSSLKSEDTALYYC---- 115
:|||||:| ||| ||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTV 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 116 VRYDHYSGSSDYWGQGTTVTVSS 138
| : ||||| ||||:
Db 121 VP-----AYWGQGTLTVSA 136

RESULT 10

US-08-976-183A-32

; Sequence 32, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9225853.2
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9315249.4
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bernhard D. Saxe
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/151/CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-976-183A-32

Query Match 74.7%; Score 537; DB 4; Length 136;
Best Local Similarity 74.8%; Pred. No. 1.5e-49;
Matches 107; Conservative 10; Mismatches 14; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGFSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC---- 115
Db 61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTV 120

Qy 116 VRYDHYSGSSDYWGQGTTVTVSS 138
Db 121 VP-----AYWGQGTLTVSA 136

RESULT 11

US-08-976-183A-34

Sequence 34, Application US/08976183A

Patent No. 6307026

GENERAL INFORMATION:

APPLICANT: King, David J.
APPLICANT: Adair, John R.
APPLICANT: Owens, Raymond J.
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K. Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;
CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/976,183A
;
; FILING DATE:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/595,848
;
; FILING DATE: 02-FEB-1996
;
; APPLICATION NUMBER: PCT/GB93/02529
;
; FILING DATE: 10-DEC-1993
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: GB 9225853.2
;
; FILING DATE: 10-DEC-1993
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 9315249.4
;
; FILING DATE: 22-JUL-1993
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Bernhard D. Saxe
;
; REGISTRATION NUMBER: 28,665
;
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202) 672-5300
;
; TELEFAX: (202) 672-5399
;
; TELEX: 904136
;
; INFORMATION FOR SEQ ID NO: 34:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 136 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein

US-08-976-183A-34

Query Match 74.5%; Score 536; DB 4; Length 136;
Best Local Similarity 74.1%; Pred. No. 1.9e-49;
Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||:||||:||||||||||||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MNFGFSLVFLVLILKGVQCEVKLVESGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC---- 115
:||||||:| ||| ||| |:|||||||:|:|:|||||||:|||||||
Db 61 EKRLIEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTV 120

Qy 116 VRYDHYSGSSDYWGQGTTVTVSS 138
| : ||||| ||||:
Db 121 VPF-----AYWGQGTLTVSA 136

RESULT 12
US-08-253-877C-57
; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:

Db 61 EKRLEWVATISGGSYTYLDSVKGRFTISRDSPRNTLYLQMSSLRSEDTALYYCAPTV 120
Qy 116 VRYDHYSGSSDYWGQGTTVTVSS 138
| : ||||| ||||:
Db 121 VPF-----AYWGQGTLVTVSA 136

RESULT 14

US-08-053-171-7

; Sequence 7, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Willaim M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-053-171-7

Query Match 74.4%; Score 535; DB 1; Length 138;
Best Local Similarity 75.4%; Pred. No. 2.5e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVCCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| || ||||| ||||| ||||| ||||| :||| ||||| ||||| :||| |||||
Db 1 MNLGLSLIFLVVLKGVCCEVKLVESGGGLVQPGGSLKLSCATSGFTFSYDYYMYWVRQTP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
:||| ||| | :||| ::| | :||| ||||| :||| ||||| | :||| :| :| |
Db 61 EKRLEWVAYISNGGGSSHYVDSVKGRFTISRDNAKNTLYLQMSRLRSEDTAMYHCARGMD 120

Qy 121 YSGSSDYWGQQTTVTVSS 138
| ||||| ||||:
Db 121 YGAWFAYWGQQTLVTVSA 138

RESULT 15

US-08-053-171-11

; Sequence 11, Application US/08053171

; Patent No. 5562903

; GENERAL INFORMATION:

; APPLICANT: Co, Loibner

; TITLE OF INVENTION: Antibody Derivatives

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-54-1

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

; LENGTH: 138 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-053-171-11

Query Match 74.4%; Score 535; DB 1; Length 138;
Best Local Similarity 75.4%; Pred. No. 2.5e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| || ||||| ||||| ||||| ||||| :||| ||||| ||||| :||| |||||:
Db 1 MNLGLSLIFLVVLKGVQCEVKLVESGGGLVQPGGSLKLSCATSGFTFSYDYYMYWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
:||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 61 EKRLEWVAYISNGGGSSHYVDSVKGRFTISRDNAKNTLYLQMSRLRSEDTAMYHCARGMD 120

Qy 121 YSGSSDYWGQQGTTVTVSS 138
| ||||| ||||:
Db 121 YGAWFAYWGQQGTLVTVSA 138

Search completed: May 17, 2004, 11:33:54
Job time : 16.8667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:25:03 ; Search time 13.8 Seconds
(without alignments)
961.915 Million cell updates/sec

Title: US-10-010-942B-4

Perfect score: 719

Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	573	79.7	138	2	S09258 Ig heavy chain V r
2	569	79.1	152	2	B26471 Ig heavy chain pre
3	559.5	77.8	139	2	S38808 Ig heavy chain - m
4	544	75.7	142	2	C34903 Ig heavy chain pre
5	521.5	72.5	140	2	S70442 Ig heavy chain pre
6	517	71.9	140	2	S31686 Ig heavy chain V r
7	516	71.8	160	2	S05271 Ig heavy chain pre
8	514	71.5	134	2	S31699 Ig heavy chain V r
9	513	71.3	140	2	S31588 Ig heavy chain V r
10	512	71.2	117	1	HVMS84 Ig heavy chain pre
11	510	70.9	117	1	HVMS34 Ig heavy chain pre
12	508	70.7	136	2	S31615 hypothetical prote
13	504	70.1	140	2	S22657 Ig heavy chain pre

14	502.5	69.9	136	1	G1MS21	Ig heavy chain pre
15	502	69.8	138	2	S31666	Ig heavy chain V r
16	501	69.7	117	1	HVMS39	Ig heavy chain pre
17	495	68.8	135	2	S31598	Ig heavy chain V r
18	493	68.6	134	2	S31679	Ig heavy chain V r
19	492.5	68.5	141	2	S31669	Ig heavy chain V r
20	492	68.4	117	1	HVMSRF	Ig heavy chain pre
21	492	68.4	139	2	I37781	Ig variable region
22	490	68.2	122	2	E27888	Ig heavy chain V r
23	487.5	67.8	119	2	F27888	Ig heavy chain V r
24	485.5	67.5	136	2	S31587	Ig heavy chain V r
25	484.5	67.4	151	2	A60943	Ig heavy chain pre
26	484	67.3	117	1	HVMS57	Ig heavy chain pre
27	484	67.3	140	2	A30532	Ig heavy chain pre
28	483	67.2	120	2	S55536	Ig heavy chain V r
29	481.5	67.0	147	2	I37780	Ig variable region
30	480.5	66.8	118	2	PH0096	Ig heavy chain V r
31	480.5	66.8	121	2	S55540	Ig heavy chain V r
32	480.5	66.8	254	2	B31790	Ig heavy chain V r
33	479	66.6	120	2	S55538	Ig heavy chain V r
34	479	66.6	120	2	S55539	Ig heavy chain V r
35	477.5	66.4	121	2	H27888	Ig heavy chain V r
36	477.5	66.4	137	2	S31701	Ig heavy chain V r
37	477.5	66.4	139	2	S31674	Ig heavy chain V r
38	476.5	66.3	137	2	S78054	Ig heavy chain pre
39	476	66.2	120	2	S55537	Ig heavy chain V r
40	473.5	65.9	118	2	PH0097	Ig heavy chain V r
41	472	65.6	132	2	S31603	Ig heavy chain V r
42	471	65.5	130	2	PL0098	Ig heavy chain pre
43	469	65.2	118	2	S20641	Ig heavy chain V r
44	467.5	65.0	135	2	I37778	Ig variable region
45	467.5	65.0	145	2	S11239	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK16.

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

RESULT 2

B26471

Ig heavy chain precursor V region (MAK33) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C;Accession: B26471; S70410
R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a
creatine-kinase-specific monoclonal antibody.
A;Reference number: A91572; MUID:87248058; PMID:3110009
A;Accession: B26471
A;Molecule type: mRNA
A;Residues: 1-152 <BUC>
A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406
R;Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 172, 1717-1727, 1990
A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary is near the promoter, and 3' boundary is about 1 kb from V(D)J gene.
A;Reference number: S70410; MUID:91079775; PMID:2258702
A;Accession: S70410
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-19 <LEB>
A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 569; DB 2; Length 152;
Best Local Similarity 78.2%; Pred. No. 3.5e-42;
Matches 111; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

Db 1 MNFGSLIIFLVVLKGVQCEVQVESGGGLVKPGGSLKLSCAAAGFTFSYDYYMYWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR-- 117
 :|||||:||| ||| |:|||||:||| ||| ||| |||:||| |||
 Db 61 EKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNLYLQMSSLKSEDTAMYYCARDKA 120
 Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138
 | :| : ||| |||:|||
 Db 121 YYGNYGDAMDYWGQGTSVTVSS 142

RESULT 3

S38808

Ig heavy chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C;Accession: S38808

R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.

Immunogenetics 36, 15-21, 1992

A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2b antibody with rheumatoid factor activity.

A;Reference number: S38807; MUID:92267566; PMID:1587549

A;Accession: S38808

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <SEQ>

A;Cross-references: EMBL:X53400

A;Note: the authors translated the codon GAG for residue 117 as Lys

A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are not shown in this paper

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 559.5; DB 2; Length 139;
 Best Local Similarity 79.3%; Pred. No. 2.1e-41;
 Matches 111; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

Qy 1 MNFGSLIIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||:|||
 Db 1 MNFGFSLIIFLVVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRDH 120
 :|||||:||| ||| |:|||||:|||:||| ||| |||:|||
 Db 61 EKRLEWVASI-SRGGTTYYPDVKGRFTISRDNAARNLYLQMSSLRSEDTAMYYCAREGI 119
 Qy 121 YSG----SSDYWGQGTTVTV 136
 | | | | |:|||
 Db 120 YYGYALYGMWDYWGQGTSVTV 139

RESULT 4

C34903

Ig heavy chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C;Accession: C34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive anti-fluorescein monoclonal antibodies.
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-142 <BED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 544; DB 2; Length 142;
Best Local Similarity 76.1%; Pred. No. 4.7e-40;
Matches 108; Conservative 9; Mismatches 21; Indels 4; Gaps 2;

Qy 1 MNFGSLIIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGFSLIIFLVLVLKGVQCEVKWVESGGLVSPGGSLKLSCAASGFTFSTYAMSWVRQTP 60

Qy 61 DKRLEWVASI--RSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY 118
Db 61 EKRLEWVASFGNKPTGGRTYYPDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARG 120

Qy 119 DHYSGS--SDYWQGQTTVTVSS 138
Db 121 GYYYGGYWFAYWQGQTLVTVSA 142

RESULT 5
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fetal B cells or a distinct B lineage?
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 521.5; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 4.1e-38;
Matches 100; Conservative 18; Mismatches 19; Indels 3; Gaps 2;

Qy 1 MNFGSLIIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MEFGLSWVFLVALLRGVQCQVQLVESGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||||| || | ||:||:|||||||:||:|||||||:||:|||:|||:|||:|||:|||:|||

Db 61 GKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-DH 119
Qy 121 YSGSS--DYWGQGTTVTVSS 138
|::: ||||||| |||||
Db 120 IVGATYFDYWGQGTLTVSS 139

RESULT 6

S31686

Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.
A;Reference number: S31585
A;Accession: S31686
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 517; DB 2; Length 140;
Best Local Similarity 70.7%; Pred. No. 9.9e-38;
Matches 99; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVCVKLVEGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| : || :|||||||:||:|||||||:|| | :|||||||:||:||| |||
Db 1 MEFGLSWLSLVAIKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||||:|| | || :|||||||:||:|||||||:||:||| :||| :|||
Db 61 GKGLEWVSAISGSGGTYYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKCPF 120
Qy 121 YSGSS--DYWGQGTTVTVSS 138
|| | ||||| |||||
Db 121 AGGSPSF DYWGQGTLTVSS 140

RESULT 7

S05271

Ig heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C;Accession: S05271; S04602
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05271
A;Molecule type: mRNA
A;Residues: 1-160 <KIS1>
A;Cross-references: EMBL:X14584


```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
       | |||| :||| :|||||||:|:||||||| || |||:|||||||:| |||||
Db      1 MEFGLSWLFLVAILKGVQCEVQLESGGGLVHPGGSIRLSCAASGFTFSSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
       | ||||:| |||:|||||:||||| |||||:|:|||||||:|||:|||||:|||:
Db      61 GKGLEWVSAISGSGGSTYYSDSVKGRLTISRDNSKNTLYLQMNSLRAEDTAVYYCARW-- 118

Qy      121 YSGSSDYWGQGTTVTVSS 138
       ||||||| |||||
Db      119 --RDLDYWGQGTLVTVSS 134

```

RESULT 9

S31588

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31588

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31588

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 513; DB 2; Length 140;
Best Local Similarity 69.3%; Pred. No. 2.2e-37;
Matches 97; Conservative 20; Mismatches 21; Indels 2; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
       | |||| :||| :|||||||:|:||||||| || |||:|||||||:| |||||
Db      1 MEFGLSWLFLVAILRGVQCEVQLESGGGLVQPFGSIRLSCAASGFTFSSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
       | ||||:| |||:|||||:||||| |||||:|:|||||||:|||:|||||:|||:
Db      61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDDSNTLYLQMNSLRAEDTAVYYCAKDHD 120

Qy      121 YSG--SSDYWGQGTTVTVSS 138
       ||| ||||||| |||||
Db      121 YSNYIYFDYWGQGTLVTVSS 140

```

RESULT 10

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0505

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.
A;Reference number: JT0501; MUID:89279149; PMID:2499654
A;Accession: JT0505
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <LEV>
A;Experimental source: strain BALB/cJ
A;Note: this sequence belongs to the VH7183 subfamily
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 71.2%; Score 512; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 2.2e-37;
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy	1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
	: :
Db	1 MNFGLSLIFLVVLKGVLCEVKLVESGGGLVQPFGSLKLSCAASGFTFSSYTMWSWVRQTP 60
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRTFISRRENAKNTLYLQMSSLKSEDTALYYCVR 117
	: : : :
Db	61 EKRLEWVAYISNGGGSTYPDTVKGRFTISRDNNAKNNLYLQMSSLKSEDTAMYYCAR 117

RESULT 11

HVMS 34

Ig heavy chain precursor V region (345) - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0502

R; Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.

A;Reference number: JT0501; MUID:89279149; PMID:2499654

A;Accession: JT0502

A;Status: translation not shown

A; Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F: 1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <TMM>

F:41-115/Disulfide bonds: #status predicted

1, II 115, bisulfide bonds. *W* *Scasas* *precautio*

Query Match 70.5%; Score 510; DB 1; Length 117;
 Best Local Similarity 83.8%; Pred. No. 3.3e-37;
 Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

A;Accession: S22657
A;Molecule type: mRNA
A;Residues: 1-140 <HIR>
A;Cross-references: EMBL:X59134
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 504; DB 2; Length 140;
Best Local Similarity 68.1%; Pred. No. 1.3e-36;
Matches 94; Conservative 21; Mismatches 19; Indels 4; Gaps 1;

Qy	1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60 : : : : : : : :
Db	1 MEFGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSSHWMTWVRQTP 60
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120 :: : : : : : :: : :
Db	61 GKRLEWVANVKQDGSAKYADSVRGRFTISRDNAKNSLYLQMDSLRAADDTAVYYCAR--- 117
Qy	121 YSGSSDYWGQGTTVTVSS 138
Db	118 -STGIDYWGQGTLVTVSS 134

RESULT 14
G1MS21
Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C;Accession: E90809; A93184; A02066
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.;
Baltimore, D.
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of
antibodies: somatic mutation evident in a gamma2a variable region.
A;Reference number: A90809; MUID:81234548; PMID:6788376
A;Accession: E90809
A;Molecule type: mRNA
A;Residues: 1-136 <BOT>
A;Cross-references: GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055
R;Adetugbo, K.; Milstein, C.; Secher, D.S.
Nature 265, 299-304, 1977
A;Title: Molecular analysis of spontaneous somatic mutants.
A;Reference number: A93184; MUID:77100368; PMID:401950
A;Contents: myeloma protein MOPC 21
A;Accession: A93184
A;Molecule type: protein
A;Residues: 17-74, 'D', 76-77, 'H', 79-88, 'ND', 91-114, 'H', 116-119, 'W', 121-136 <ADE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>
F;31-114/Domain: immunoglobulin homology <IMM>
F;115-119/Region: D segment

F;120-136/Region: J segment (JH4)
F;38-112/Disulfide bonds: #status experimental

Query Match 69.9%; Score 502.5; DB 1; Length 136;
 Best Local Similarity 70.4%; Pred. No. 1.7e-36;
 Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

Db 62 EEWVAYISSLHYADTVKGRETISRDNPKNTLFLQMTSLRSEDTAMYCARWGNYPYY 121

Qy 124 SSDYWGQGTTVTVSS 138
: :||||||:|||||
Db 122 AMDYWGQGTSVTVSS 136

RESULT 15

S31666

Ig heavy chain V region - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31666

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A; Reference number: S31585

A;Accession: S31666

A; Status: preliminary

A; Molecule type: mRNA

A;Residues: 1-138 <CUI>

A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 502; DB 2; Length 138;
Best Local Similarity 67.6%; Pred. No. 1.9e-36;
Matches 96; Conservative 21; Mismatches 17; Indels 8; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKGASLKLSCAASGFTFSNYGMSWVRQNS 60
| :||| :||| :|||||:|:|||||:||| :|||||:||| :||| :|||
Db 1 MEGFLSWLFLVAILKGVOCEVOLLESGGGLVOPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRTTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
 | | | |::| | | |::|:| | | | | | | |::| | | | | | | |::| | | | | | | :
 Pb 61 CKCIEVVAISGSGCSTKXADSVKGRTTISRDNSKNLTYLQMNSI RAEDTAVVYCAKART 120

61 GRGLEWVSAISGGSYYADSVKGRFTISRDNSRKNLYLQMNSLRAEDTAVYICARAT 120

QY 118 -YDHYSGSSSDYWQGQGTTVTVSS 138
| ::| ||:|| |||||
Db 121 GYWYF----DLWGRGTLTVSS 138

Search completed: May 17, 2004, 11:33:09
Job time : 14.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:32:34 ; Search time 39.3556 Seconds
(without alignments)
975.722 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVVLKGVQCE.....DHYSGGSSDYWGQQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	719	100.0	138	14	US-10-010-942B-4	Sequence 4, Appli
2	719	100.0	138	16	US-10-388-389-4	Sequence 4, Appli
3	652	90.7	138	14	US-10-010-942B-8	Sequence 8, Appli
4	652	90.7	138	16	US-10-388-389-8	Sequence 8, Appli
5	650	90.4	138	14	US-10-010-942B-12	Sequence 12, Appli
6	650	90.4	138	16	US-10-388-389-12	Sequence 12, Appli
7	609.5	84.8	133	13	US-10-006-773-9	Sequence 9, Appli
8	578.5	80.5	139	13	US-10-006-773-17	Sequence 17, Appli
9	578	80.4	462	14	US-10-281-479A-23	Sequence 23, Appli
10	578	80.4	462	14	US-10-286-132A-23	Sequence 23, Appli
11	578	80.4	464	14	US-10-275-180A-23	Sequence 23, Appli
12	569	79.1	144	9	US-09-881-823-12	Sequence 12, Appli
13	566	78.7	140	9	US-09-286-240-4	Sequence 4, Appli
14	559	77.7	140	13	US-10-006-773-4	Sequence 4, Appli
15	557.5	77.5	137	9	US-09-423-800-76	Sequence 76, Appli
16	557.5	77.5	137	14	US-10-337-981-76	Sequence 76, Appli
17	553	76.9	158	12	US-10-226-795-32	Sequence 32, Appli
18	549	76.4	140	14	US-10-283-349-23	Sequence 23, Appli
19	542	75.4	140	12	US-10-365-123-51	Sequence 51, Appli
20	537	74.7	159	15	US-10-291-265-333	Sequence 333, App
21	531.5	73.9	143	11	US-09-791-551-117	Sequence 117, App
22	522	72.6	313	15	US-10-291-265-427	Sequence 427, App
23	522	72.6	470	16	US-10-038-591-46	Sequence 46, Appli
24	520.5	72.4	469	12	US-10-292-088-54	Sequence 54, Appli
25	514.5	71.6	139	10	US-09-947-839-96	Sequence 96, Appli
26	514	71.5	138	9	US-09-796-744-15	Sequence 15, Appli
27	514	71.5	138	14	US-10-231-452-62	Sequence 62, Appli
28	512	71.2	465	14	US-10-401-344-2	Sequence 2, Appli
29	510.5	71.0	137	9	US-09-423-800-77	Sequence 77, Appli
30	510.5	71.0	137	14	US-10-337-981-77	Sequence 77, Appli
31	510.5	71.0	473	16	US-10-038-591-50	Sequence 50, Appli
32	508.5	70.7	307	15	US-10-291-265-332	Sequence 332, App
33	508.5	70.7	363	15	US-10-291-265-335	Sequence 335, App
34	506	70.4	474	10	US-09-848-832-3	Sequence 3, Appli
35	506	70.4	474	14	US-10-225-108A-3	Sequence 3, Appli
36	506	70.4	474	15	US-10-461-148-1	Sequence 1, Appli
37	503.5	70.0	471	12	US-10-292-088-6	Sequence 6, Appli
38	503	70.0	312	15	US-10-291-265-334	Sequence 334, App
39	503	70.0	470	12	US-10-292-088-62	Sequence 62, Appli
40	500.5	69.6	137	15	US-10-443-466A-45	Sequence 45, Appli
41	500	69.5	470	16	US-10-038-591-45	Sequence 45, Appli
42	500	69.5	470	16	US-10-038-591-49	Sequence 49, Appli
43	499	69.4	367	15	US-10-291-265-899	Sequence 899, App
44	498.5	69.3	467	12	US-10-180-648-2	Sequence 2, Appli
45	498	69.3	140	15	US-10-443-466A-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1

US-10-010-942B-4

; Sequence 4, Application US/10010942B

; Publication No. US20030165496A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Guriq

; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4

Query Match 100.0%; Score 719; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.5e-61;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
||| ||| ||| ||| ||| |||
Db 121 YSGSSDYWGQGTTVTVSS 138

RESULT 2

US-10-388-389-4
; Sequence 4, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||| ||| ||| :| :| :| :| :| :| :|
Db 1 MNFGLSLIFLVVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||| ||| ||| ||| ||| :| :| :| :| :| :|
Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
| ||| ||| ||| |||
Db 121 YSGSSDYWGQGTLVTVSS 138

RESULT 4

US-10-388-389-8

; Sequence 8, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)

US-10-388-389-8

Query Match 90.7%; Score 652; DB 16; Length 138;
Best Local Similarity 89.1%; Pred. No. 2.1e-54;
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||| ||| ||| :| :| :| :| :| :| :|
Db 1 MNFGLSLIFLVVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||| ||| ||| ||| ||| :| :| :| :| :|
Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
| ||| ||| ||| |||

; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 light chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)

US-10-388-389-12

RESULT 7

US-10-006-773-9

; Sequence 9, Application US/10006773

; Publication No. US20020132983A1

; GENERAL INFORMATION:

; APPLICANT: Junghans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antigens

: FILE REFERENCE: 003

FILE REFERENCES: CURRENT APPLICATION

CURRENT APPLICATION NUMBER: 09/10,300,773

PRIOR APPLICATION NUMBER: 60/350

PRIOR APPLICATION NUMBER: 80/250
PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30
NAME OF SEC. ID: NGS_10

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Mus sp.

US-10-006-773-9

```

Query Match          84.8%;  Score 609.5;  DB 13;  Length 133;
Best Local Similarity  87.0%;  Pred. No. 2.2e-50;
Matches 120;  Conservative 6;  Mismatches 7;  Indels 5;  Gaps 1;

Qy      1 MNFGLSLIFLVVLKGVCQEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
       |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||| |
Db      1 MNFGLSLIFLVVLKGVCQEVKVVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
       |||||||:|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||| |
Db      61 DKRLEWVASISSGGDSTFYADNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCARDDL 120

Qy      121 YSGSSDYWGQGTTTVVSS 138
       ::: |||||:||| |
Db      121 FN----WGQGTTLTIVSS 133

```

RESULT 8

US-10-006-773-17
; Sequence 17, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US 10 006 773 17

US-10-006-773-17

US-10-286-132A-23

; Sequence 23, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e
= Synthetic Construct

US-10-286-132A-23

Query Match 80.4%; Score 578; DB 14; Length 462;
Best Local Similarity 81.2%; Pred. No. 8.9e-47;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy	1 MNFGLSLIFLVVLKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
	:
Db	1 MNFGLSLIFLVVLKGVCQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
	: : : : : :
Db	61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYCCARRGD 120
Qy	121 YSGSSDYWGQGTTVTVSS 138
	:: :
Db	121 SMITTDYWGQGTTLTVSS 138

RESULT 11

US-10-275-180A-23

; Sequence 23, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.

; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS-
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U5
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1
=
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-23

Query Match 80.4%; Score 578; DB 14; Length 464;
Best Local Similarity 81.2%; Pred. No. 9e-47;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFLVVLKGVCQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 EKRLRWVATISSGGSYTYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGD 120

Qy 121 YSGSSDYWGQGTTTVSS 138
Db 121 SMITTDYWGQGTTLTVSS 138

RESULT 12
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 144

; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-12

Query Match 79.1%; Score 569; DB 9; Length 144;
Best Local Similarity 78.2%; Pred. No. 1.7e-46;
Matches 111; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:|||||:||||| |||||||:||||| ||| |||||||:| |||
Db 1 MDFGLSLVFLVLTKGVQCDVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMWSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
:||||||| ||| ||| :|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EKRLEWVASISSGGTYTYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCSRDDG 120

Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138
| | : |||||||:|||||
Db 121 SYGSYYYAMDYWGQGTSVTVSS 142

RESULT 13

US-09-286-240-4

; Sequence 4, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Fett, James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 10498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-286-240-4

Query Match 78.7%; Score 566; DB 9; Length 140;
Best Local Similarity 79.3%; Pred. No. 3.2e-46;
Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:|||||:||||| ||||||| ||| |||||||:| |||
Db 1 MDFGLSWVFLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMWSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY-D 119
:|||||||:| ||| ||| :|||||:|||||:|||||:|||||:|||||:| |||
Db 61 EKRLEWVATISSGGGNTYYPDSVKGRFTISRDIAKNTLYLQMSSLRSEDTALYYCTRLGD 120

Qy 120 H-YSGSSDYWGQGTTVTVSS 138
: | : |||||||:|||||
Db 121 YGYAYTMDYWGQGTSVTVSS 140

RESULT 14

US-10-006-773-4
; Sequence 4, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-4

Query Match 77.7%; Score 559; DB 13; Length 140;
Best Local Similarity 77.9%; Pred. No. 1.5e-45;
Matches 109; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVCCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGFSLIFLVVLKGVCCEVVVVESGGFVKPGGSLKLSCAAAGFTFSRYAMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR-Y 118
Db 61 EKRLIEWVATISSGGSHTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAIYYCARPGY 120

Qy 119 DHYSGSSDYWGQGTTVTVSS 138
Db 121 DRGAWFFDVWGAGTTVTVSS 140

RESULT 15
US-09-423-800-76
; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-76

Query Match 77.5%; Score 557.5; DB 9; Length 137;
Best Local Similarity 78.3%; Pred. No. 2e-45;
Matches 108; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| ||||| ||| :||| ||||| :||| ||| ||| ||| ||| ||| ||| :||| ||| :|||
Db 1 MNFGLSLIFLALILKGVCQCEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMWSWIRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
||| ||||| :| ||| ||| | :||| ||||| :||| ||| ||| ||| ||| :| :| |
Db 61 DKRLEWVATISSGGSYTYYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMFYCARQTT 120

Qy 121 YSGSSDYWGQQGTTVTVSS 138
: : ||| ||| ||| :
Db 121 MTYFA-YWGQGTLVTVSA 137

Search completed: May 17, 2004, 11:42:06
Job time : 40.3556 secs

1	576.5	80.2	487	11	Q99KA4	Q99ka4 mus musculu
2	557	77.5	479	11	Q91WP5	Q91wp5 mus musculu
3	547	76.1	486	11	Q91Z07	Q91z07 mus musculu
4	516.5	71.8	473	11	Q91Z05	Q91z05 mus musculu
5	505	70.2	480	11	Q91XE1	Q91xe1 mus musculu
6	503	70.0	597	4	Q96BB9	Q96bb9 homo sapien
7	492	68.4	119	11	Q920E7	Q920e7 mus musculu
8	490	68.2	499	4	Q8N5K4	Q8n5k4 homo sapien
9	486.5	67.7	613	4	Q8WUK1	Q8wuk1 homo sapien
10	483.5	67.2	573	4	Q8WU38	Q8wu38 homo sapien
11	471	65.5	493	4	Q8NCL6	Q8nc16 homo sapien
12	461.5	64.2	494	4	Q96K68	Q96k68 homo sapien
13	449	62.4	470	4	Q7Z5W1	Q7z5w1 homo sapien
14	448	62.3	487	11	Q80ZI7	Q80zi7 mus musculu
15	435.5	60.6	469	11	Q8R3V9	Q8r3v9 mus musculu
16	429	59.7	113	4	Q9UL90	Q9ul90 homo sapien
17	426.5	59.3	479	11	Q7TMK4	Q7tmk4 mus musculu
18	418	58.1	121	4	Q9UL71	Q9ul71 homo sapien
19	417.5	58.1	484	11	Q8VEA0	Q8vea0 mus musculu
20	414.5	57.6	112	4	Q9HCC1	Q9hcc1 homo sapien
21	412.5	57.4	147	4	Q9Y509	Q9y509 homo sapien
22	411.5	57.2	118	4	Q9UL91	Q9ul91 homo sapien
23	409.5	57.0	437	11	Q9R1A4	Q9rla4 mus musculu
24	407	56.6	482	4	Q7Z351	Q7z351 homo sapien
25	405	56.3	116	4	Q9UL93	Q9ul93 homo sapien
26	402	55.9	521	4	Q8N4Y9	Q8n4y9 homo sapien
27	401.5	55.8	298	11	Q9QYF0	Q9qyf0 mus musculu
28	397.5	55.3	122	4	Q9UL84	Q9ul84 homo sapien
29	393.5	54.7	118	4	Q9UL72	Q9ul72 homo sapien
30	385	53.5	131	4	Q9UL88	Q9ul88 homo sapien
31	368	51.2	95	4	Q9ULB6	Q9ulb6 homo sapien
32	364	50.6	473	11	Q9D8L4	Q9d8l4 mus musculu
33	351	48.8	168	11	Q8VDC9	Q8vdc9 mus musculu
34	350.5	48.7	463	11	Q99LC4	Q99lc4 mus musculu
35	349	48.5	468	11	Q99L31	Q99l31 mus musculu
36	348	48.4	470	11	Q7TMK1	Q7tmk1 mus musculu
37	348	48.4	484	11	Q99LA6	Q99la6 mus musculu
38	343.5	47.8	145	11	Q924Q7	Q924q7 mus musculu
39	343.5	47.8	482	11	Q8K172	Q8k172 mus musculu
40	340.5	47.4	124	6	Q9N0W4	Q9n0w4 oryctolagus
41	339.5	47.2	278	11	Q921K1	Q921k1 mus musculu
42	337.5	46.9	124	6	Q9N0W6	Q9n0w6 oryctolagus
43	337	46.9	481	11	Q91WT1	Q91wt1 mus musculu
44	336.5	46.8	124	4	Q9UL92	Q9ul92 homo sapien
45	336	46.7	117	11	Q9QXE9	Q9qxe9 mus musculu

ALIGNMENTS

RESULT 1

Q99KA4

ID Q99KA4 PRELIMINARY; PRT; 487 AA.
 AC Q99KA4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 80.2%; Score 576.5; DB 11; Length 487;
Best Local Similarity 79.2%; Pred. No. 1.3e-47;
Matches 114; Conservative 7; Mismatches 16; Indels 7; Gaps 2;

Qy	1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
	: :	
Db	1 MNFGLSLIFLVLVLKGVQCEVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP	60
	: : :	
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR---	117
	: : : :	
Db	61 EKRLEWVATISDGGSYTYYPDNVKGRTFTISRDNAKNNLYLQMSHLKS EDTAMYYCARDMG	120
	:	
Qy	118 ---YDHYSGSSDYWGQGTTVTVSS	138
	:	
Db	121 GSPYGGYS-RFDYWGQGTTITVSS	143

RESULT 2

Q91WP5
ID Q91WP5 PRELIMINARY; PRT; 479 AA.
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

 Query Match 77.5%; Score 557; DB 11; Length 479;
 Best Local Similarity 78.3%; Pred. No. 9.8e-46;
 Matches 108; Conservative 10; Mismatches 16; Indels 4; Gaps 1;

 Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:|||||| |||||||:||||||||| |||:|||||| |||||:|||||||:
 Db 1 MNFGLTIFLVLTLKGVQCEVQLVESGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 :|||||||:|| | || ||| :|||||||:|||:|||||||:||||| |||||:
 Db 61 EKRLEWVAAINSNGGNTYYSDTMKGRFTISRDNAKSTLYLQMSSLRSEDTAFYYCVR-- 117

 Qy 121 YSGSSDYWGQGTTVTVSS 138
 | | ||| |||||||:
 Db 118 -GGYFDVWGAGTAVTVSS 134

RESULT 3
 Q91Z07
 ID Q91Z07 PRELIMINARY; PRT; 486 AA.
 AC Q91Z07;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC010324; AAH10324.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

 Query Match 76.1%; Score 547; DB 11; Length 486;
 Best Local Similarity 76.2%; Pred. No. 9.3e-45;
 Matches 109; Conservative 12; Mismatches 16; Indels 6; Gaps 3;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| ||||||| ||||||||| ||||||||| ||||| ||||:||:|| |||||
 Db 1 MNFGLRLIFLVLALKGVQCEVHLVESGGGLVKPGGSLKLSCVVGFSFTSYDMSWVRQTP 60
 ||||| ||||||| ||||||||| ||||| ||||:||:|| |||||
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRD- 119
 ::|||||||:| ||| ||| |||||||||:|||:||| |||||||||:|||:||| :
 Db 61 ERRLEWVAITS-GGNTYYPDNVKGRFTSRDNAKYTLYLQMSSLKSEDTAMYYCVRPEI 119
 ||||| ||||||| ||||||||| ||||| ||||:|||:|||
 Qy 120 ---HYSGS-SDYWQGTTTVTVSS 138
 :||||| | |||||||:|||||
 Db 120 PIYYYSGSYFDSWGQGTTITVSS 142

RESULT 4

Q91Z05

ID Q91Z05 PRELIMINARY; PRT; 473 AA.
 AC Q91Z05;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN AU044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC010327; AAH10327.1; -.
 DR MGD; MGI:2144967; AU044919.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 71.8%; Score 516.5; DB 11; Length 473;
 Best Local Similarity 72.5%; Pred. No. 8.3e-42;
 Matches 100; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |: |:||||:|||||||:|||||||:||| |||||||||:||| |||||
 Db 1 MDSRLNLVFLVLALKGVQCEVQLVESGGGLVKPGGSRKLSCAASGFTFSYGMHWVRQAP 60
 ||||| ||||||| ||| |||:||| |||||||||:|||:|||:|||:|||:||| :
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRD- 120
 ||||| ||||||| ||| |||:||| |||||||||:|||:|||:|||:|||:||| :
 Db 61 EKGLEWVAYINSGTTIYYADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCAR-EL 119

Qy 121 YSGSSDYWGQGTTVTVSS 138
: |||||||:|||||
Db 120 WLRRIDYWGQGTTITVSS 137

RESULT 5

Q91XE1

ID Q91XE1 PRELIMINARY; PRT; 480 AA.
AC Q91XE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010798; AAH10798.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 70.2%; Score 505; DB 11; Length 480;
Best Local Similarity 72.3%; Pred. No. 1.1e-40;
Matches 99; Conservative 16; Mismatches 20; Indels 2; Gaps 1;

Qy 2 NFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSD 61
:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 NFGLSLIFLVVLKGVLCDVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTP 60

Qy 62 KRLEWVASIRSGGGRTYYSDNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCVRYDHY 121
:|||||:|:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 61 KRLEWVATISNSGYATHYPDSMKGRFTISRDNAQNTVLLQMTSILNSEDTAVYYCTRGDYW 120

Qy 122 SGSSDYWGQGTTVTVSS 138
| || |||||||
Db 121 --YFDVWGAGTTVTVSS 135

RESULT 6

Q96BB9

ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 70.0%; Score 503; DB 4; Length 597;
Best Local Similarity 66.7%; Pred. No. 2.3e-40;
Matches 96; Conservative 22; Mismatches 20; Indels 6; Gaps 2;

RESULT 7

Q920E7

ID Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed

RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
DR PIR; C25913; C25913.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1 1
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 68.4%; Score 492; DB 11; Length 119;
Best Local Similarity 79.0%; Pred. No. 3.7e-40;
Matches 94; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
||:||||||| ||||| ||||||| |||:||||||| |||||||||:| ||| |||||
Db 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY 60
Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYSGSSDYWGQGTTVTVSS 138
|:|||||||:|||:|||||||||:|||||:||| |: | ||| ||||| |||||:
Db 61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHGDYDVGFAWGQGTLTVSA 119

RESULT 8

Q8N5K4

ID Q8N5K4 PRELIMINARY; PRT; 499 AA.
AC Q8N5K4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC032249; AAH32249.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 68.2%; Score 490; DB 4; Length 499;
Best Local Similarity 67.1%; Pred. No. 3.3e-39;
Matches 98; Conservative 16; Mismatches 24; Indels 8; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :||||||:||||||:||| :||:|||| |||| :| |||||
Db 1 MEFGLSWVFLVAILKGVQCEVQLVESGGGVVRPGSRLSCATSGFTFDDSGASWVRQAP 60
| ||||:||| ||| :|||:||||||:||||:|||:|||:|||:|||:|||
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--Y 118
| ||||:||| ||| :|||:||||||:||||:|||:|||:|||:|||
Db 61 GKGLEWVSSINWNGGSTNYADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPT 120
| ||||:||| ||| :|||:||||||:||||:|||:|||:|||:|||
Qy 119 DHYSGSS-----DYWGQGTTVTVSS 138
: ||| | | ||:|||||||
Db 121 KYCSGGSCLGYYMDVWGKGTTVTVSS 146

RESULT 9

Q8WUK1

ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 67.7%; Score 486.5; DB 4; Length 613;
Best Local Similarity 67.9%; Pred. No. 9.4e-39;
Matches 95; Conservative 19; Mismatches 23; Indels 3; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :||:||||:|||:||||||:||| :||:|||||||:||| |||||
Db 1 MEFGLSWVFLVALLRGVQCQVQLVESGGGVQPGRSRLSCAASGFTFSSYGMHWVRQAP 60
| ||||:||| ||| :|||:||||||:||||:|||:|||:|||:|||:|||
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRDH 120

Db	<pre> ::: ::: ::: : </pre> 61 GKGLEWVAVI SYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-DW 119
Qy	121 YSG--SSDYWGQGTIVTVSS 138 <pre> : </pre>
Db	120 SEGVETFDIWGQGTMVTVSS 139

RESULT 10

Q8WU38

ID Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR PIR; S21205; S21205.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 67.2%; Score 483.5; DB 4; Length 573;
 Best Local Similarity 66.9%; Pred. No. 1.7e-38;
 Matches 97; Conservative 15; Mismatches 24; Indels 9; Gaps 2;

Qy	1	MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
		: : : : : :	
Db	1	MELGLSWIFLLAIIKGVQCEVOLVESGGGLVQPGRSRLSCAASGFTFDDYAMHWVRQAP	60

Qy	61	DKRLEWVASIRSGGGRTYYSDNVKGRTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH	120
		: : : : : : : : : : : : :	
Pb	61	GKGLEWVSGISWNSGSISGYADSVKGRTISRDNAKNSLYLOMNSLRAEDTALYYCAK--H	118

QY	121	YSGS-----SDYWQGTTVTVSS	138
Pb	119	GGSYSYIGYYYGMDVWGOGTTVTVSS	143

RESULT 11

Q8NCL6

ID Q8NCL6 PRELIMINARY; PRT; 493 AA.

AC Q8NCL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK074651; BAC11114.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 65.5%; Score 471; DB 4; Length 493;
Best Local Similarity 65.0%; Pred. No. 2.3e-37;
Matches 91; Conservative 19; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :||:||||:||:||||||:|| |||:||||||| | :||| ||||:
Db 1 MQFGLSWVFLVALLRGVQCQVQLVESGGGVLPGGSLRLSCAASGFRFRDYDMHWVRQSP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
: ||||| | | :||||:|||| |:|||: ||||||:|| | :||||:||| |
Db 61 GEGLEWVALIWYDGTKTYYSDSVKGRLTVSRDNYKNTLYLEMKSLGAEDTAVYYCARDQG 120

Qy 121 YSGSS--DYWGQGTTVTVSS 138
|:| |:||||| |||||
Db 121 YAGYGVFDHWGQGTLTVSS 140

RESULT 12

Q96K68

ID Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK027379; BAB55072.1; -.
DR PIR; S21205; S21205.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEE4C0E CRC64;

Query Match 64.2%; Score 461.5; DB 4; Length 494;
Best Local Similarity 65.5%; Pred. No. 1.9e-36;
Matches 93; Conservative 16; Mismatches 28; Indels 5; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| || :||| |:|||||:|||||:|||||:||:|||||:||| | :|||
Db 1 MELGLRWVFLVAFLEGVQCEVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||||:|| | || | :|||||:|||||:|||||:||: :|||:||| | |
Db 61 GKGLEWVSSSISSRSYIYYRDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYCAR-DS 119

Qy 121 YSGSSDY----WGQGTTVTVSS 138
:|: | ||||| |||||
Db 120 CNGAICYGFSPWGQGTLVTVSS 141

RESULT 13

Q7Z5W1
ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC053984; AAH53984.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 62.4%; Score 449; DB 4; Length 470;
 Best Local Similarity 63.8%; Pred. No. 3e-35;
 Matches 90; Conservative 20; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | ||| :|||:||:|||||:|||||:||| ||:||| ||||| :||| |||
 Db 1 MELGLSWVFLVVILEGVQCEVQLVESGGGLVQPGGSLRLSCVASGFTLNNYDMHWVRQGI 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR-YD 119
 | ||||: | : | | ||: :|||||||||:||| ||:||: | | :||| |
 Db 61 GKGLEWVSKIGTAGDR-YYAGSVKGRFTISRENAKDSLQLQMNSLRVGDAAVYYCARGAG 119

 Qy 120 HYS--GSSDYWGQGTTVTVSS 138
 :: |: | ||||| |||||
 Db 120 RWAPLGAFDIWGQGTMVTVSS 140

RESULT 14

Q80ZI7
 ID Q80ZI7 PRELIMINARY; PRT; 487 AA.
 AC Q80ZI7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC049143; AAH49143.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Query Match 62.3%; Score 448; DB 11; Length 487;
Best Local Similarity 61.3%; Pred. No. 3.9e-35;
Matches 87; Conservative 26; Mismatches 25; Indels 4; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| ||: :||:| :||||| |||| |:||||||:|| |:||||| ||||| |:||||:
Db 1 MYLGLNCVFIGFLLKGVQSEVKLEEAGGLVQPGGSMKLSCAASGFTFSNYWMNWVRQSP 60

Qy 61 DKRLEWVASI--RSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR- 117
:| ||||| | || |:|:||:|||||||::|:||:|:||:|:| :||| |
Db 61 EKGLEWVAEIRLRSNNYATHYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRR 120

Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138
| : | || |||||||
Db 121 GYGDPNWYFDVWGAGTTVTVSS 142

RESULT 15
Q8R3V9
ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC024405; AAH24405.1; -.
 DR PIR; B45837; B45837.
 DR MGD; MGI:96446; Ig-h-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

 Query Match 60.6%; Score 435.5; DB 11; Length 469;
 Best Local Similarity 61.6%; Pred. No. 6.2e-34;
 Matches 90; Conservative 22; Mismatches 25; Indels 9; Gaps 4;

 Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | |: |||| :| :||||| |||||||||:|| ||:|||||||:|| |||||||
 Db 1 MKLWLWNWIFLVTLLNGIQCEVNLVESGGGLVQPGGSLRLSCAASGFTFTDYYMSWVRQPP 60

 Qy 61 DKRLEWVASIR--SGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR- 117
 | |||: || :| | || :|||||||:||::: |||||:||::||:| ||| |
 Db 61 GKALEWLGFIRNKANGYTTEYSASVKGRFTISRDNSQSILYLQMNALRAEDSATYYCARD 120

 Qy 118 ----YDHYSGSS-DYWGQGTTVTVSS 138
 | :|||:| ||||||| ||||:
 Db 121 RRSSY-YYSGTSFAYWGQGTLTVSA 145

Search completed: May 17, 2004, 11:32:30
 Job time : 37.2889 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:11:13 ; Search time 10.2222 Seconds
(without alignments)
702.947 Million cell updates/sec

Title: US-10-010-942B-4

Perfect score: 719

Sequence: 1 MNFGLSLIFLVLVLKGKVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	512	71.2	117	1	HV54_MOUSE P18525 mus musculu
2	510	70.9	117	1	HV55_MOUSE P18526 mus musculu
3	502.5	69.9	136	1	HV16_MOUSE P01783 mus musculu
4	501	69.7	117	1	HV59_MOUSE P18530 mus musculu
5	492	68.4	117	1	HV53_MOUSE P18524 mus musculu
6	484	67.3	117	1	HV58_MOUSE P18529 mus musculu
7	463	64.4	117	1	HV3C_HUMAN P01764 homo sapien
8	433.5	60.3	116	1	HV05_CARAU P19181 carassius a
9	427	59.4	142	1	HV01_RAT P01805 rattus norv
10	426	59.2	144	1	HV26_MOUSE P01795 mus musculu
11	418.5	58.2	97	1	HV56_MOUSE P18527 mus musculu
12	417	58.0	121	1	HV3J_HUMAN P01771 homo sapien
13	414	57.6	98	1	HV57_MOUSE P18528 mus musculu
14	412.5	57.4	122	1	HV3G_HUMAN P01768 homo sapien
15	406.5	56.5	116	1	HV3T_HUMAN P01781 homo sapien
16	402.5	56.0	119	1	HV40_MOUSE P01810 mus musculu
17	400.5	55.7	119	1	HV37_MOUSE P01807 mus musculu

18	397.5	55.3	116	1	HV36_MOUSE	P01806 mus musculu
19	396.5	55.1	111	1	HV35_MOUSE	P01804 mus musculu
20	395.5	55.0	119	1	HV38_MOUSE	P01808 mus musculu
21	393	54.7	117	1	HV02_CANFA	P01785 canis famil
22	388	54.0	118	1	HV39_MOUSE	P01809 mus musculu
23	387.5	53.9	122	1	HV20_MOUSE	P01789 mus musculu
24	386	53.7	115	1	HV32_MOUSE	P01801 mus musculu
25	385.5	53.6	122	1	HV3A_HUMAN	P01762 homo sapien
26	385	53.5	113	1	HV30_MOUSE	P01799 mus musculu
27	384.5	53.5	126	1	HV3K_HUMAN	P01772 homo sapien
28	384	53.4	119	1	HV3L_HUMAN	P01773 homo sapien
29	382.5	53.2	122	1	HV21_MOUSE	P01790 mus musculu
30	382	53.1	115	1	HV3F_HUMAN	P01767 homo sapien
31	381.5	53.1	114	1	HV3B_HUMAN	P01763 homo sapien
32	380.5	52.9	122	1	HV3H_HUMAN	P01769 homo sapien
33	380	52.9	123	1	HV18_MOUSE	P01787 mus musculu
34	379	52.7	113	1	HV27_MOUSE	P01796 mus musculu
35	379	52.7	120	1	HV3E_HUMAN	P01766 homo sapien
36	378	52.6	115	1	HV33_MOUSE	P01802 mus musculu
37	378	52.6	123	1	HV19_MOUSE	P01788 mus musculu
38	378	52.6	123	1	HV22_MOUSE	P01791 mus musculu
39	377	52.4	113	1	HV31_MOUSE	P01800 mus musculu
40	374	52.0	117	1	HV41_MOUSE	P01811 mus musculu
41	373	51.9	113	1	HV28_MOUSE	P01797 mus musculu
42	372	51.7	119	1	HV3I_HUMAN	P01770 homo sapien
43	372	51.7	123	1	HV23_MOUSE	P01792 mus musculu
44	371	51.6	117	1	HV42_MOUSE	P01812 mus musculu
45	371	51.6	123	1	HV24_MOUSE	P01793 mus musculu

ALIGNMENTS

RESULT 1

HV54_MOUSE

ID HV54_MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/cJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0505; HVMS84.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 71.2%; Score 512; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 1.4e-44;
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFLVVLKGVLCEVKLVESGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
Db 61 EKRLEWVAYISNGGGSTYYDPDTVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR 117

RESULT 2
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

 Query Match 70.9%; Score 510; DB 1; Length 117;
 Best Local Similarity 83.8%; Pred. No. 2.2e-44;
 Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

 Qy 1 MNFGLSLIFLVVLKGVCVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| ||||| ||||:|||:||||||||| ||||| ||:|| |||||
 Db 1 MNFGLRLIFLVTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 :||||||| | ||||| ||| | |||||||:|||||||||:|||||
 Db 61 EKRLEWVAYISSGGGSTYYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR 117

RESULT 3
 HV16_MOUSE
 ID HV16_MOUSE STANDARD; PRT; 136 AA.
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NP^b family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RX MEDLINE=77100368; PubMed=401950;
 RA Adetugbo K., Milstein C., Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants.";
 RL Nature 265:299-304(1977).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; J00522; AAD15290.1; -.
 DR PIR; E90809; G1MS21.
 DR PDB; 1IGC; 03-JUN-95.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT NON_TER 1 1
 FT SIGNAL <1 16
 FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
 FT DOMAIN 115 119 D SEGMENT.
 FT DOMAIN 120 136 JH4 SEGMENT.
 FT DISULFID 38 112
 FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).
 FT CONFLICT 115 115 W -> H (IN REF. 2).
 FT CONFLICT 120 120 Y -> W (IN REF. 2).
 FT NON_TER 136 136
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 69.9%; Score 502.5; DB 1; Length 136;
 Best Local Similarity 70.4%; Pred. No. 1.5e-43;
 Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

Qy 124 SSDYWGQGTTVTVSS 138
: |||||||:|||||
Pb 122 AMDYWGQGTTVTVSS 136

RESULT 4

RESULTS

ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;

RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0507; HVMS39.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 69.7%; Score 501; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 1.8e-43;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFVLILKGVQCEVKWVESGGGSVKPGGSLKLSCEASGFTFSNYGMSWVRQTP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
Db 61 EKRLEWVASISGGVSYTYYPDSVKGRFTISRDNAKNLYLQMNSLTSEDTALYYCAR 117

RESULT 5
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0503; HVMSRF.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 68.4%; Score 492; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 1.4e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLRLIFLVLVLKGVLCDVKLVESGGGLVKLGGSILKLSCAASGFTFSSYYMSWVRQTP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
Db 61 EKRLELVAAINSNGGSTYYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCAR 117

RESULT 6
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR HSSP; P01810; 2FBJ.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

 Query Match 67.3%; Score 484; DB 1; Length 117;
 Best Local Similarity 79.5%; Pred. No. 9e-42;
 Matches 93; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

 Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||| ||||| |:||||||| ||||||||||| ||||| |||||:| |||||
 Db 1 MNFVLSLIFLALILKGVQCEVHLVESGGGLVKPGGSLKLSCVSGFTFNKYAMSWVRQTP 60

 Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 :|||||||:| ||| ||| |:|||||||||:||| |||||||||:|||||:|||
 Db 61 EKRLEWVATISSGGLYTYYPDSVKGRFTISRDNAGNTLYLQMSSLRSEDTAMYCAR 117

RESULT 7
 HV3C_HUMAN
 ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Matthysse G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 RT heavy chain variable region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR PDB; 1HOU; 23-DEC-99.
DR Genew; HGNC:5545; IGHV@.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 64.4%; Score 463; DB 1; Length 117;
Best Local Similarity 72.6%; Pred. No. 1.2e-39;
Matches 85; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :|||||||:|:|||||||:||| :|||||||:|:|||||||
Db 1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60
Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
| ||||:| ||| :|||||||:|:|||||||:||| :| ||| :||| :
Db 61 GKGLEWVSAISGSGGSTYYGDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117

RESULT 8
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR HSSP; P01772; 2FB4.

RESULT 9
HV01_RAT
ID HV01_RAT STANDARD; PRT; 142 AA.
AC P01805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region IR2 precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
RT E.";
RL Nucleic Acids Res. 10:6041-6049(1982).
CC -!- MISCELLANEOUS: THE mRNA WAS ISOLATED FROM AN IGE-SECRETING
CC IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02075; EVRTR2.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
FT DOMAIN 20 133 IG-LIKE.
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 59.4%; Score 427; DB 1; Length 142;
Best Local Similarity 58.3%; Pred. No. 6e-36;
Matches 84; Conservative 23; Mismatches 29; Indels 8; Gaps 3;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|: |: :|:| :| ||| ||| ||| ||| :||| :|:||| ||| ||| :| | |||
Db 1 MDLRLTYVFIVAILKGVLCEVKLEESGGGLVQPGMSVKLSCATSGFTFSDYWMEMWVRQAP 60

Qy 61 .DKRLEWVASIRSGGGR--TYYSDNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCVRY 118
| ||||| ||: ||| ::|||||:||:||:|:|:||| ||:::||| :||| |||
Db 61 GKGLEWVAEIRNKANNYVAYYGKSLKGRTFLSRDDSKSIVYLQMNNIRSEDTGIYYCSR- 119

Qy 119 DHYSGSSD----YWQGQTTVTVSS 138
| | |: ||| |||
Db 120 -GYGGYSENWFVYWGQGTLTVSS 142

RESULT 10

HV26_MOUSE
ID HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01795;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101208;
RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";
RL Cell 27:573-581(1981).
RN [2]
RP SEQUENCE OF 20-142.
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS PHOSPHORYLCHOLINE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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DR EMBL; J00516; AAC18867.2; ALT_TERM.

DR PIR; A90818; AVMS67.

DR HSSP; P01789; 1MCP.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.

FT DOMAIN 20 133 IG-LIKE.

FT CONFLICT 125 125 N -> D (IN REF. 2).

FT NON_TER 144 144

SQ SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;

Query Match 59.2%; Score 426; DB 1; Length 144;

Best Local Similarity 58.3%; Pred. No. 7.6e-36;

Matches 84; Conservative 23; Mismatches 31; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASILKLSAASGFTFSNYGMSWVRQNS 60
| | : :||: :| :|:||||:|||||:||| ||:|||| |||||:| |||

Db 1 MKMWLNWVFLTLHGIQCEVKVVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQTP 60

Qy 61 DKRLEWVASIRSGGG--RTYYSDNVKGRTFISRENAKNTLYLQMSSLKSEDTALYYCVR- 117
| |||:|:||| ||| :|:||| :||| :|:||| :|:||| :|:||| :|:||| :|:|||

Db 61 GKRLEWIAASRSKAHDYRTEYSASVKGRFIVSRDTSQSVLYLQMNALRAEDTATYYCTRD 120

Qy 118 ---YDHYSGSSDYWGQGTTVTVSS 138

:| | | ||| |||||||||

Db 121 ADYGNSYFGYFDVWGAGTTVTVSS 144

RESULT 11

HV56_MOUSE

ID HV56_MOUSE STANDARD; PRT; 97 AA.

AC P18527;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region 914.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/cJ;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; JT0504; HVMS91.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >97 IG-LIKE.
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

 Query Match 58.2%; Score 418.5; DB 1; Length 97;
 Best Local Similarity 82.7%; Pred. No. 2.8e-35;
 Matches 81; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

 Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 ||||||| ||||| ||||| :| ||||| :||||| ||||| |||||
 Db 1 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLWVASI-SSGGSTYY 59

 Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 :|||||:|||:|||:|||:|||:|||:|||:|||
 Db 60 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYCAR 97

RESULT 12
 HV3J_HUMAN
 ID HV3J_HUMAN STANDARD; PRT; 121 AA.
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region HIL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 RT cryoimmunoglobulin IgG Hil.";
 RL Biochemistry 18:553-560(1979).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02054; G1HUHL.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

 Query Match 58.0%; Score 417; DB 1; Length 121;
 Best Local Similarity 66.1%; Pred. No. 5e-35;
 Matches 80; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

 Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 ::|||::|::|::|::|| ||:||| ||||||||||| ||||| | ||||| | | |||||
 Db 1 QVKLVQAGGGVVQPGRSRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY 60

 Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRVDHY--SGSSDYWGQGTTVTVS 137
 |:|||||||:|::| |||::|:||:||| | : | ||||| | |||||
 Db 61 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGVLTIVS 120

 Qy 138 S 138
 |
 Db 121 S 121

RESULT 13
 HV57_MOUSE
 ID HV57_MOUSE STANDARD; PRT; 98 AA.
 AC P18528;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 6.96.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/cJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; JT0501; HVMS96.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 >98 IG-LIKE.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 57.6%; Score 414; DB 1; Length 98;
Best Local Similarity 80.6%; Pred. No. 7.9e-35;
Matches 79; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
||:||||||||||| |||||||||||||:|| ||| :|||||||:|| |||
Db 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSYYMYWVRQTPEKRLEWVATISDGGSYTY 60

Qy 80 SDNVKGRTTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
|:|||||||:|||| |||||||||||||:|||
Db 61 PDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR 98

RESULT 14

HV3G_HUMAN

ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 57.4%; Score 412.5; DB 1; Length 122;
Best Local Similarity 64.2%; Pred. No. 1.4e-34;

Matches 79; Conservative 19; Mismatches 20; Indels 5; Gaps 2;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 :|:|||||||:|:|| ||:||||||| | |||| | ||||| | | ||

Db 1 QVELVESGGGVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 60

Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR---YDHYSGSSDYWGQGTTVT 135
 :::|||||||:|::|:|||||||:||:|:||| | | | :| ||||| ||

Db 61 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYR-AFNYWGQGTLVT 119

Qy 136 VSS 138
 |||

Db 120 VSS 122

RESULT 15

HV3T_HUMAN

ID HV3T_HUMAN STANDARD; PRT; 116 AA.
 AC P01781;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 RT type), subgroup H III. Architecture of the complete IgM-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [2]
 RP REVISION TO 28-33.
 RA Hilschmann N.;
 RL Submitted (JUN-1975) to the PIR data bank.
 CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02064; M3HUGL.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 56.5%; Score 406.5; DB 1; Length 116;
Best Local Similarity 67.2%; Pred. No. 5.4e-34;
Matches 80; Conservative 13; Mismatches 23; Indels 3; Gaps 1;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
||:|||||| ||:|| ||:|||||| | : ||:|||| | |||||:|: | | |

Db 1 EVQLVESGGDLVQPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGSZBY 60

Qy 80 SDNVKGRTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYSGSSDYWGQGTTVTVSS 138
|:|||||||:||||:||||:||: |||||| | | | ||||| | | |

Db 61 VDSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCAR---GWGGGDYWGQGTLVTVST 116

Search completed: May 17, 2004, 11:31:05

Job time : 10.2222 secs